

Figure 1A

1 CGTCCGGCGGGGCGCAGGGCTGAGCGAGCGTCCGGGCTCCGGGGCTCCGGGGAAGCGGT 60  
 61 TGCAGCTCCTGAGTGCAGCGCGGCTTCCTGCCACTGTCCCGGCCCGCCACCTCTCTGTCT 120  
 121 ATGGCTCTGGCGGACAGCACACGTGGATTACCCAACGGGGGCGGCGCGGGGGCGGCAGT 180  
 1 M A L A D S T R G L P N G G G G G G G S 20  
 181 GGCTCCTCGTCTCTCCGCGGAGCCACCGCTCTTCCCCGACATCGTGGAGCTGAACGTG 240  
 21 G S S S S S A E P P L F P D I V E L N V 40  
 241 GGGGGCCAGGTGTACGTGACCCGCGCTGCACGGTGGTGTGCGTGCCCGACTCGCTGCTC 300  
 41 G G Q V Y V T R R C T V V S V P D S L L 60  
 301 TGGCGCATGTTACGCGAGCAGCGCCGAGAGCTGGCCCGGACAGCAAGGCGCGTTC 360  
 61 W R M F T Q Q Q P Q E L A R D S K G R F 80  
 361 TTTCTGGACCGGGACGGCTTCCTCTTCCGCTACATCCTGGATTACCTGCGGGACTTGCAG 420  
 81 F L D R D G F L F R Y I L D Y L R D L Q 100  
 421 CTCGTGCTGCCCCGACTACTTCCCCGAGCGCAGCCGGCTGCAGCGCGAGGCCGAGTACTTC 480  
 101 L V L P D Y F P E R S R L O R E A E Y F 120  
 481 GAGCTGCCAGAGCTCGTGCGCCGCTCGGGGCGCCCCAGCAGCCCGGCCGGGGCGCCGG 540  
 121 E L P E L V R R L G A P Q Q P G P G P P 140  
 541 CCCTCGCGCGCGGGGGTGCAAGGAGGGCTCGCTGGGTGACGAGCTGCTGCGCGTTGGC 600  
 141 P S R R G V H K E G S L G D E L L P L G 160  
 601 TACTCGGAGCCCGAAGCAGCAGGAGGGCGCTCTGCGGGGCGCCGTCGCCACGCTGGAG 660  
 161 Y S E P E Q Q E G A S A G A P S P T L E 180  
 661 CTGGCTAGCCGAGTCCGTCGCGGGGCGGCGGGGCCGCTGCTACGCGCTCCAGTCTG 720  
 181 L A S R S P S G G A A G P L L T P S Q S 200  
 721 CTGGACGCGAGCCGCGCTCGGGCTACATCACCATCGGCTACCGCGGCTTCTACACCATC 780  
 201 L D G S R R S G Y I T I G Y R G S Y T I 220  
 781 GGGCGGGACGCGCAGGCGGACGCCAAGTTCCGGCGAGTGGCGCGCATCACCGTTTTCGCGA 840  
 221 G R D A Q A D A K F R R V A R I T V C G 240  
 841 AAGACGTCGCTGGCCAAGGAGGTGTTTGGGGACACCTGAACGAAAGCGGGACCCCGAC 900  
 241 K T S L A K E V F G D T L N E S R D P D 260

Figure 1B

901	CGTCCCCCGAGCGCTACACCTCGCGCTATTACCTCAAGTTCAACTTCCTGGAGCAGGCC	960
261	R P P E R Y T S R Y Y L K F N F L E Q A	280
961	TTCGACAAGCTGTCCGAGTCGGGCTTCCACATGGTGGCGTGCAGCTCCACGGGCACCTGC	1020
281	F D K L S E S G F H M V A C S S T G T C	300
1021	GCCTTTGCCAGCAGCACCACAGAGCGAGGACAAGATCTGGACCAGTACACCGAGTAC	1080
301	<u>A F A</u> S S T D Q S E D K I W T S Y T E Y	320
1081	GTCTTCTGCAGGGAGTGAGCTCCCCAGACCCCTCGCCACTCCAGCGCCAGTCCTTCTC	1140
321	V F C R E	325
1141	CTGCCCGAGAGATGATTACAGAGCCTCTTGTCACACCTTTGTCCCTGGCTGCTGCCCTC	1200
1201	CCATTCTCCCCCTCCAGTAGTAGCTGGGTGAGACCTGTCCGCCACCTTCCCTCCACTAC	1260
1261	AGAACCTGCAGCCGCAAACTCTCTGGGCTGCTTCGTCTTCTTTGGACCTCCTGAACCGAG	1320
1321	AGAAGCCAGAGGAACCCCAACCCCAACCCCACTACCACCTCCATGCTTCTCTACTCCCT	1380
1381	GCCTCAAACACCCCTCCCCCAGATGGTACTTCAGTTTGGATCTATTGGGGGAGTGTGGC	1440
1441	CACAGACCGGGGATGATTGAATTGTTTCAGAACCTGATTGGACCGTGCCAATGTGCGGA	1500
1501	AGATTTCCTTGAAATCTTCTCAAGCTCTTATGACTCACTGGGGGTTAAGAGATCAGGAT	1560
1561	TGGTTCCACTGTCTGGGGT <sup>+</sup> AGTGT <sup>+</sup> TTTACAAGGTCATTACACAGTCTTTT <sup>+</sup> TGACCTCT <sup>+</sup>	1620
1621	TTGAAGGTAGAGTTT <sup>+</sup> TAGAAGGCTGGATGGAAGATTCTGAGCCTGGAATTAGGACCCCAT	1680
1681	GGAGGCAGTCC <sup>+</sup> TCAAACCA <sup>+</sup> CCCTCCCCCAGATGGTACTTCAGTTTGGATCTAT <sup>+</sup> TGGGGG	1740
1741	AGTGTGGCCACAGACCGGGGATGATTGAATTGTTTCAGAACCTGATTGGACCGTGCCAA	1800
1801	TGTGCGGAAGATTTCCTTGA <sup>+</sup> AATCTTCTCAAGCTCTTATGACTCACTGGGGGT <sup>+</sup> TAAGAG	1860
1861	ATCAGGATTGGTTCCACTGTCTGGGGT <sup>+</sup> TAGTGT <sup>+</sup> TTTACAAGGTCATTACACAGTCTTTT <sup>+</sup>	1920
1921	GACCTCTTTTGAAGGTAGAGTTT <sup>+</sup> TAGAAGGCTGGATGGAAGATTCTGAGCCTGGAATTAG	1980

**Figure 1C**

1981 GACCCCATGGAGGCAGTTCAGTAACTAACTAATAAAGTTTGAAAAGTTACACGTAAAA 2040  
2041 AAAAAAAAAAAAA 2052

D0121 NP

Figure 2A

		1	50
K+betaM6	(1)	MALADSTRGLPNGGGGGGSGSSSS	AEPLFPDIVELVNCGGVYVRRC
KCNMB1	(1)	-----	-----MVKKLVMAQKRGETRALCLGVTAVVCAMITYYILVAVTL
K+Hnov27	(1)	---MSRPLITRSPASPLXNQGITPTP	QLTKSNAPVHIIDVGGHNYSSLR
K+Hnov28	(1)	-----	-----MDNGDWGYMHTDPVILNVGGHLYVTSLT
KIAA1317	(1)	---QQQKGTMALSGNCSRYYPREQGS	AVPNSPFEVVLNVGGQVYVRHGS
CG10465	(1)	-----	-----MSEMSGDHKLILKGHSQYILNVGGHLYVMTIG
CG10830	(1)	-----	-----MPLEITLVNCGVSYVTHLA
K+channel_tetra	(1)	-----	-----MTSVEVTLNVGGTLYVTHGS
		51	100
K+betaM6	(51)	AVVSV	PDSLLEWRMFTQQ---QPOELANDSKRFFELDRDQFLFRYILDYI
KCNMB1	(40)	ELVYK	SVVWTQESKCHLIETNIRDQEEELKGHVPQPCLVNVMVSAAGRWA
K+Hnov27	(47)	RTTKY	ESRIRGRIGDTEP-----IYLDSEIQQHVEIDRDQFLFRYINFL
K+Hnov28	(29)	RTTRY	PDSLLEWAMPQSDFP-----TPRQPCENVEIDRDQFLFRYVNF
KIAA1317	(49)	PLISD	PSLLWKMFPKPR--DTANDLAKDSKRFETDRDQFLFRYILDYI
CG10465	(36)	RLTKNN	DTMLGAMESGR-----MEVLTQSEGMILLDRCNHGGITILNVI
CG10830	(20)	RLQDR	STLTAELGEG-----RDSLAKDSKRFELDRDQFLFRYILDYI
K+channel_tetra	(23)	RLSKR	ETLTAELASSSLSSEDOANVVTLTDTTLVDRDQFLFRYVHFI
		101	150
K+betaM6	(97)	RLCL	VLDPYRPFERSRLQREAFYFELPELVRRIGAPQPGSGPPPSRGV
KCNMB1	(90)	LYHT	EDTRDQNGQCSYIPGSVDNYGTARADVEKVRARKEQEQ-----
K+Hnov27	(92)	RTSKL	LIPDLTKDYMLVEBAKYFQIQPMLEMERWKQDEPT-----
K+Hnov28	(73)	RTSEL	LIPDLTKDYMLVEBAKYFQIQPMLEMERWKQDEPT-----
KIAA1317	(97)	RDRQ	VLDPYRPFERSRLQREAFYFELPELVRRIGAPQPGSGPPPSRGV
CG10465	(80)	RDGT	VLDPYRPFERSRLQREAFYFELPELVRRIGAPQPGSGPPPSRGV
CG10830	(65)	RCKAL	MLPBGERRRRLLEAEHFRITAMLECHRSERDARE-----
K+channel_tetra	(73)	RTDKL	SLPBGERRRRLLEAEHFRITAMLECHRSERDARE-----
		151	200
K+betaM6	(147)	HKEG	SLGDELLPLGYSEPEQEGASAGAPSPITLEASRSPSGGAAGPLIT
KCNMB1	(132)	-----	-----
K+Hnov27	(134)	-----	-----
K+Hnov28	(114)	-----	-----
KIAA1317	(139)	-----	-----DEFCHSDFEDASQ-----GSDTRICP
CG10465	(130)	LITS	QKEQLLLSVSLKPAVILVVQRQNN-----KYSTYSTS
CG10830	(106)	-----	-----P-----
K+channel_tetra	(114)	-----	-----RPRTANG
		201	250
K+betaM6	(197)	PSQSL	DGSRRSGLTGGYRGSYTIQRDAQADAKFRFVARITVCGKTSIAK
KCNMB1	(132)	-----	-----VFYCSAPRGNETSVLVFORLYGQALLFSLFWPFIITGGLL
K+Hnov27	(134)	-----	-----GRFSRQCELVVRVAPDLGERITLSGDKSLIDEEVFETG
K+Hnov28	(114)	-----	-----MDTFEEVVLESTRKLKSYSNPVAIVITQITVTKVHSL
KIAA1317	(160)	PSLL	PADRKWCGLTVGYRGSCTLCREGQADAKFRFVARITVCGKTSIAK
CG10465	(121)	DDNLL	KNIELDFKLIRFNERILFTKDVITPSEICCSWFYGHGKVAVC
CG10830	(107)	-----	-----SCITGGYRGSFQFGKGLADVKFRKLSRLTVCORVAOCR
K+channel_tetra	(121)	YNTIT	SGETGCTVTLGYRC-----
		251	300
K+betaM6	(247)	SVFG	DTLNESSRDPDRP-PEPYTSRYVYKFNFLQAFDKLSESCSHMVACS
KCNMB1	(174)	IDAM	VKSNQOYLSILAQK-----
K+Hnov27	(173)	IVMC	NSVAGWNHGSTHVIHPPLNGYCHLNSVOVLERLQ-DRCHFEVNSC
K+Hnov28	(154)	IGIS	NYETKWKHMMDTDRDQVSTFEGPCDYHGEVSLRVHLMEMITKQGF
KIAA1317	(210)	SVFG	DTLNESSRDPDRP-PEPYTSRYVYKFNFLQAFDKLSESCSHMVACS
CG10465	(121)	CNSI	VATDRKHVVEFPARIYEETQVLLYENRNAPQDLMOATSSAR
CG10830	(146)	SVFG	DTLNESSRDPDGGTDRTYTSRFFELKHCVLEQAFDNLHDCVYRMAGSC
K+channel_tetra	(141)	-----	-----

Figure 2B

```

301                                     350
K+betaM6 (296) STGTCAFASST---DQSEDMIWTSYTEYVFCRE-----
KCNMB1 (192) -----
K+Hnov27 (222) GGGVDSSQFSEYVLRRELRRTPRVPSVIRIKQEPL-----
K+Hnov28 (204) TIRNTRVHHMSERANENTVEHNWTECRLARKTDD-----
KIAA1317 (259) SSVTASFIN----QYTPDKIWSSTTEYVFYREPSRWSPSHCDCCCKNGK
CG10465 (267) VGSASGTSINQYTSDEEEERTGLARLSNKRNMPS-----
CG10830 (196) GSGTAGSAAEPKPGVDTEENRWNTENEVFVIRE-----
K+channel_tetra (141) -----

351                                     400
K+betaM6 (326) -----
KCNMB1 (192) -----
K+Hnov27 (257) -----
K+Hnov28 (238) -----
KIAA1317 (304) GDKEGESGTSNDLSTSSCDQSSEASSPQETVICGPVTRQTNIQTLDRPI
CG10465 (302) -----
CG10830 (229) -----
K+channel_tetra (141) -----

401                                     450
K+betaM6 (326) -----
KCNMB1 (192) -----
K+Hnov27 (257) -----
K+Hnov28 (238) -----
KIAA1317 (354) KKGFPVQLIQSEMRKSDLLRTLTSGSRESNMSSKKKAVKEKLSIEEELE
CG10465 (302) -----
CG10830 (229) -----
K+channel_tetra (141) -----

451                                     482
K+betaM6 (326) -----
KCNMB1 (192) -----
K+Hnov27 (257) -----
K+Hnov28 (238) -----
KIAA1317 (404) KCIQDFLKIKIPDRFPERKHPWQSELLRKYHL
CG10465 (302) -----
CG10830 (229) -----
K+channel_tetra (141) -----

```

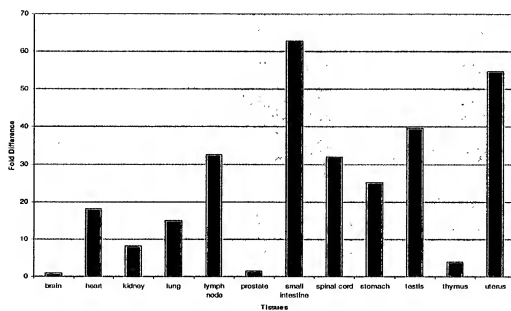
**Figure 3**

Figure 4.

<u>Protein</u>	<u>Genbank / SWISS- PROT Accession No.</u>	<u>Identities</u>	<u>Similarities</u>
human Maxi-K potassium channel beta subunit, KCNMB1 protein	gil4758625	0.0%	37.5%
human potassium channel K+Hnov27 protein	gilY34125	30.21%	39.15%
human potassium channel K+Hnov28 protein	gilY34129	30.04%	38.63%
Caenorhabditis elegans K+ channel tetramerisation domain containing protein	gil3880445	31.11%	39.26%
Drosophila CG10465 protein	gil17946205	23.9%	33.0%
Drosophila CG10830 protein	gil7300672	50.89%	62.5%
human KIAA1317 protein	gil7243015	60.42%	69.97%

Figure 5

